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RAW SEQUENCE LISTING

DATE: 03/19/2002

PATENT APPLICATION: US/10/087,217

TIME: 14:16:13

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\03192002\J087217.raw

#2

3 <110> APPLICANT: Aptus Genomics, Inc.
4 YAO, Yong
5 CAO, Liang
7 <120> TITLE OF INVENTION: Novel Cell-Based Assays for G-Protein-Coupled Receptor-Mediated
8 Activities
10 <130> FILE REFERENCE: 53735-5004-US
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/087,217
C--> 12 <141> CURRENT FILING DATE: 2002-03-04
12 <150> PRIOR APPLICATION NUMBER: 60/330,663
13 <151> PRIOR FILING DATE: 2001-10-26
15 <160> NUMBER OF SEQ ID NOS: 8
17 <170> SOFTWARE: PatentIn version 3.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1995
21 <212> TYPE: DNA
22 <213> ORGANISM: Rattus norvegicus
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (1)..(1992)
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35 cat aac cat cat cct cct cct tct atc aag gcc aat ggc aaa gat gac 96
36 His Asn His His Pro Pro Pro Ser Ile Lys Ala Asn Gly Lys Asp Asp
37 20 25 30
39 cac agg gca gga agc aga cca cag tct gtg gca gct gat gat gac act 144
40 His Arg Ala Gly Ser Arg Pro Gln Ser Val Ala Ala Asp Asp Asp Thr
41 35 40 45
43 tct cca gaa cta caa agg ctg gca gag atg gat acc cct cgg agg ggg 192
44 Ser Pro Glu Leu Gln Arg Leu Ala Glu Met Asp Thr Pro Arg Arg Gly
45 50 55 60
47 agg ggt ggc ttc caa agg att gtt cgc ctg gtg ggg gtc atc agg gac 240
48 Arg Gly Gly Phe Gln Arg Ile Val Arg Leu Val Gly Val Ile Arg Asp
49 65 70 75 80
51 tgg gcc aac aag aat ttc cgt gaa gag gaa cca agg cct gac tcc ttc 288
52 Trp Ala Asn Lys Asn Phe Arg Glu Glu Glu Pro Arg Pro Asp Ser Phe
53 85 90 95
55 cta gag cgt ttc cgt ggg cca gaa ctc cag act gtg aca acc cat cag 336
56 Leu Glu Arg Phe Arg Gly Pro Glu Leu Gln Thr Val Thr Thr His Gln
57 100 105 110
59 ggg gat gac aaa ggc ggc aag gac ggc gag gga aag ggc acc aaa aag 384

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63 aaa ttt gaa ctg ttt gtt ttg gac cca gcc gga gac tgg tat tac cgt      432
64 Lys Phe Glu Leu Phe Val Leu Asp Pro Ala Gly Asp Trp Tyr Tyr Arg
65      130      135      140
67 tgg ttg ttt gtc att gcc atg cct gtt ctt tac aac tgg tgc ctg ttg      480
68 Trp Leu Phe Val Ile Ala Met Pro Val Leu Tyr Asn Trp Cys Leu Leu
69 145      150      155      160
71 gtg gcc aga gcc tgc ttc agt gat cta cag aga aac tat ttt gtg gta      528
72 Val Ala Arg Ala Cys Phe Ser Asp Leu Gln Arg Asn Tyr Phe Val Val
73      165      170      175
75 tgg ctg gtg ctg gac tac ttc tca gac act gtc tat atc gca gac ctc      576
76 Trp Leu Val Leu Asp Tyr Phe Ser Asp Thr Val Tyr Ile Ala Asp Leu
77      180      185      190
79 atc att cgg ctg cgc aca ggc ttc cta gaa cag ggg ctc ttg gtc aaa      624
80 Ile Ile Arg Leu Arg Thr Gly Phe Leu Glu Gln Gly Leu Leu Val Lys
81      195      200      205
83 gat ccc aag aaa ttg cga gac aac tat att cac act ttg cag ttc aaa      672
84 Asp Pro Lys Lys Leu Arg Asp Asn Tyr Ile His Thr Leu Gln Phe Lys
85      210      215      220
87 ttg gat gtg gct tct atc att ccc act gac ctt atc tat ttt gct gtg      720
88 Leu Asp Val Ala Ser Ile Ile Pro Thr Asp Leu Ile Tyr Phe Ala Val
89 225      230      235      240
91 ggt atc cac agc cct gag gta cgc ttc aac cgt cta tta cac ttt gcc      768
92 Gly Ile His Ser Pro Glu Val Arg Phe Asn Arg Leu Leu His Phe Ala
93      245      250      255
95 cgt atg ttt gag ttc ttt gac cgc act gag aca cgc acc agc tac ccc      816
96 Arg Met Phe Glu Phe Phe Asp Arg Thr Glu Thr Arg Thr Ser Tyr Pro
97      260      265      270
99 aac atc ttc cga atc agc aat ctg gtc ctt tac atc ttg gtc atc atc      864
100 Asn Ile Phe Arg Ile Ser Asn Leu Val Leu Tyr Ile Leu Val Ile Ile
101      275      280      285
103 cac tgg aat gct tgt att tat tat gtt att tct aag tcc att ggc ttt      912
104 His Trp Asn Ala Cys Ile Tyr Tyr Val Ile Ser Lys Ser Ile Gly Phe
105      290      295      300
107 gga gtt gac acc tgg gtt tac ccc aac att act gac cct gaa tat ggc      960
108 Gly Val Asp Thr Trp Val Tyr Pro Asn Ile Thr Asp Pro Glu Tyr Gly
109 305      310      315      320
111 tac ctg gct aga gag tac att tac tgt ctt tac tgg tcc aca ctg acc      1008
112 Tyr Leu Ala Arg Glu Tyr Ile Tyr Cys Leu Tyr Trp Ser Thr Leu Thr
113      325      330      335
115 ctc acc acc att gga gag aca cca ccc cct gta aag gat gag gag tac      1056
116 Leu Thr Thr Ile Gly Glu Thr Pro Pro Pro Val Lys Asp Glu Glu Tyr
117      340      345      350
119 cta ttt gtc atc ttt gac ttc ttg att ggt gtc ctc atc ttt gcc act      1104
120 Leu Phe Val Ile Phe Asp Phe Leu Ile Gly Val Leu Ile Phe Ala Thr
121      355      360      365
123 att gtg gga aat gtg ggc tcc atg atc tcc aac atg aat gcc aca cga      1152
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128	Ala Glu Phe Gln Ala Lys Ile Asp Ala Val Lys His Tyr Met Gln Phe			
129	385 390 395 400			
131	cga aag gtc agc aaa gac atg gaa gcc aag gtc atc aaa tgg ttt gac	1248		
132	Arg Lys Val Ser Lys Asp Met Glu Ala Lys Val Ile Lys Trp Phe Asp			
133	405 410 415			
135	tac ttg tgg acc aat aag aag aca gta gat gaa cga gaa gtc ctc aag	1296		
136	Tyr Leu Trp Thr Asn Lys Lys Thr Val Asp Glu Arg Glu Val Leu Lys			
137	420 425 430			
139	aac ctg cca gca aag ctc agg gct gag ata gcc att aat gtt cac ttg	1344		
140	Asn Leu Pro Ala Lys Leu Arg Ala Glu Ile Ala Ile Asn Val His Leu			
141	435 440 445			
143	tcc act ctg aag aaa gtg cgc ata ttc cag gat tgt gaa gct ggc cta	1392		
144	Ser Thr Leu Lys Lys Val Arg Ile Phe Gln Asp Cys Glu Ala Gly Leu			
145	450 455 460			
147	ctg gtg gaa ctg gta ctg aag ctt cgt cct cag gtc ttt agt cct gga	1440		
148	Leu Val Glu Leu Val Leu Lys Leu Arg Pro Gln Val Phe Ser Pro Gly			
149	465 470 475 480			
151	gat tat att tgc cgt aag ggg gac att ggc aag gaa atg tac atc atc	1488		
152	Asp Tyr Ile Cys Arg Lys Gly Asp Ile Gly Lys Glu Met Tyr Ile Ile			
153	485 490 495			
155	aag gag ggc aag ttg gca gtg gta gct gat gat ggc gtg act cag tat	1536		
156	Lys Glu Gly Lys Leu Ala Val Val Ala Asp Asp Gly Val Thr Gln Tyr			
157	500 505 510			
159	gcc ttg ctc tca gct ggg agc tgc ttt ggt gag att agt atc ctt aac	1584		
160	Ala Leu Leu Ser Ala Gly Ser Cys Phe Gly Glu Ile Ser Ile Leu Asn			
161	515 520 525			
163	att aag ggt agc aaa atg ggc aat cga cgt act gct aat atc cgt agc	1632		
164	Ile Lys Gly Ser Lys Met Gly Asn Arg Arg Thr Ala Asn Ile Arg Ser			
165	530 535 540			
167	ctg ggc tac tca gat ctc ttc tgc ttg tcc aag gac gat ctt atg gaa	1680		
168	Leu Gly Tyr Ser Asp Leu Phe Cys Leu Ser Lys Asp Asp Leu Met Glu			
169	545 550 555 560			
171	gct gta act gag tat cct gat gcc aag aag gtc ctg gag gaa cgg ggt	1728		
172	Ala Val Thr Glu Tyr Pro Asp Ala Lys Lys Val Leu Glu Glu Arg Gly			
173	565 570 575			
175	agg gag atc ctg atg aag gaa ggt cta ctg gat gag aat gaa gtg gca	1776		
176	Arg Glu Ile Leu Met Lys Glu Gly Leu Leu Asp Glu Asn Glu Val Ala			
177	580 585 590			
179	gct agt atg gag gta gat gtt cag gag aag ctg gaa cag ttg gag aca	1824		
180	Ala Ser Met Glu Val Asp Val Gln Glu Lys Leu Glu Gln Leu Glu Thr			
181	595 600 605			
183	aac atg gat acc ttg tac act cgc ttt gcc cgc ctg ctg gct gag tac	1872		
184	Asn Met Asp Thr Leu Tyr Thr Arg Phe Ala Arg Leu Leu Ala Glu Tyr			
185	610 615 620			
187	act ggg gcc cag cag aag ctc aag caa cgc atc aca gtg cta gag acc	1920		
188	Thr Gly Ala Gln Gln Lys Leu Lys Gln Arg Ile Thr Val Leu Glu Thr			
189	625 630 635 640			

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216          35          40          45
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224 65          70          75          80
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228          85          90          95
231 Leu Glu Arg Phe Arg Gly Pro Glu Leu Gln Thr Val Thr Thr His Gln
232          100         105         110
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236          115         120         125
239 Lys Phe Glu Leu Phe Val Leu Asp Pro Ala Gly Asp Trp Tyr Tyr Arg
240          130         135         140
243 Trp Leu Phe Val Ile Ala Met Pro Val Leu Tyr Asn Trp Cys Leu Leu
244 145          150         155         160
247 Val Ala Arg Ala Cys Phe Ser Asp Leu Gln Arg Asn Tyr Phe Val Val
248          165         170         175
251 Trp Leu Val Leu Asp Tyr Phe Ser Asp Thr Val Tyr Ile Ala Asp Leu
252          180         185         190
255 Ile Ile Arg Leu Arg Thr Gly Phe Leu Glu Gln Gly Leu Leu Val Lys
256          195         200         205
259 Asp Pro Lys Lys Leu Arg Asp Asn Tyr Ile His Thr Leu Gln Phe Lys
260          210         215         220
263 Leu Asp Val Ala Ser Ile Ile Pro Thr Asp Leu Ile Tyr Phe Ala Val
264 225          230         235         240
267 Gly Ile His Ser Pro Glu Val Arg Phe Asn Arg Leu Leu His Phe Ala
268          245         250         255
271 Arg Met Phe Glu Phe Phe Asp Arg Thr Glu Thr Arg Thr Ser Tyr Pro
272          260         265         270
275 Asn Ile Phe Arg Ile Ser Asn Leu Val Leu Tyr Ile Leu Val Ile Ile
276          275         280         285
279 His Trp Asn Ala Cys Ile Tyr Tyr Val Ile Ser Lys Ser Ile Gly Phe
280          290         295         300

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283 Gly Val Asp Thr Trp Val Tyr Pro Asn Ile Thr Asp Pro Glu Tyr Gly
284 305 310 315 320
287 Tyr Leu Ala Arg Glu Tyr Ile Tyr Cys Leu Tyr Trp Ser Thr Leu Thr
288 325 330 335
291 Leu Thr Thr Ile Gly Glu Thr Pro Pro Pro Val Lys Asp Glu Glu Tyr
292 340 345 350
295 Leu Phe Val Ile Phe Asp Phe Leu Ile Gly Val Leu Ile Phe Ala Thr
296 355 360 365
299 Ile Val Gly Asn Val Gly Ser Met Ile Ser Asn Met Asn Ala Thr Arg
300 370 375 380
303 Ala Glu Phe Gln Ala Lys Ile Asp Ala Val Lys His Tyr Met Gln Phe
304 385 390 395 400
307 Arg Lys Val Ser Lys Asp Met Glu Ala Lys Val Ile Lys Trp Phe Asp
308 405 410 415
311 Tyr Leu Trp Thr Asn Lys Lys Thr Val Asp Glu Arg Glu Val Leu Lys
312 420 425 430
315 Asn Leu Pro Ala Lys Leu Arg Ala Glu Ile Ala Ile Asn Val His Leu
316 435 440 445
319 Ser Thr Leu Lys Lys Val Arg Ile Phe Gln Asp Cys Glu Ala Gly Leu
320 450 455 460
323 Leu Val Glu Leu Val Leu Lys Leu Arg Pro Gln Val Phe Ser Pro Gly
324 465 470 475 480
327 Asp Tyr Ile Cys Arg Lys Gly Asp Ile Gly Lys Glu Met Tyr Ile Ile
328 485 490 495
331 Lys Glu Gly Lys Leu Ala Val Val Ala Asp Asp Gly Val Thr Gln Tyr
332 500 505 510
335 Ala Leu Leu Ser Ala Gly Ser Cys Phe Gly Glu Ile Ser Ile Leu Asn
336 515 520 525
339 Ile Lys Gly Ser Lys Met Gly Asn Arg Arg Thr Ala Asn Ile Arg Ser
340 530 535 540
343 Leu Gly Tyr Ser Asp Leu Phe Cys Leu Ser Lys Asp Asp Leu Met Glu
344 545 550 555 560
347 Ala Val Thr Glu Tyr Pro Asp Ala Lys Lys Val Leu Glu Glu Arg Gly
348 565 570 575
351 Arg Glu Ile Leu Met Lys Glu Gly Leu Leu Asp Glu Asn Glu Val Ala
352 580 585 590
355 Ala Ser Met Glu Val Asp Val Gln Glu Lys Leu Glu Gln Leu Glu Thr
356 595 600 605
359 Asn Met Asp Thr Leu Tyr Thr Arg Phe Ala Arg Leu Leu Ala Glu Tyr
360 610 615 620
363 Thr Gly Ala Gln Gln Lys Leu Lys Gln Arg Ile Thr Val Leu Glu Thr
364 625 630 635 640
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376 <211> LENGTH: 1995
377 <212> TYPE: DNA

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VERIFICATION SUMMARY

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PATENT APPLICATION: US/10/087,217

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date